WHAT IS CLAIMED IS:

1. A method for predicting nucleic acid hybridization thermodynamics, the method comprising:

providing a database of thermodynamics parameters;

receiving hybridization information which represents at least one sequence;

receiving correction data;

receiving a first set of data which represents hybridization conditions; and

calculating hybridization thermodynamics including net hybridization thermodynamics based on the hybridization information, the thermodynamic parameters, the correction data and the first set of data.

2. The method as claimed in claim 1 wherein the hybridization thermodynamics of individual single stranded, bimolecular and higher order complexes are statistically weighted in a numerical process and the equilibrium concentration of each species is output.

3. The method as claimed in claim 2 wherein the correction data includes folding correction data.

4. The method as claimed in claim 2 wherein the correction data includes linear correction data.

5. The method as claimed in claim 1 wherein the thermodynamic parameters include DNA thermodynamic parameters.

6. The method as claimed in claim 5 wherein the DNA thermodynamic parameters include dangling end parameters.

7. The method as claimed in claim 5 wherein the DNA thermodynamic parameters include coaxial stacking parameters.

8. The method as claimed in claim 5 wherein the DNA thermodynamic parameters include terminal mismatch parameters.

9. The method as claimed in claim 1 wherein the thermodynamic parameters include RNA thermodynamic parameters.

10. The method as claimed in claim 1 wherein the thermodynamic parameters include hybrid DNA/RNA thermodynamic parameters.

11. The method as claimed in claim 1 wherein the thermodynamic parameters include DNA loop thermodynamic parameters.

12. The method as claimed in claim 1 wherein the hybridization information represents top and bottom strand sequences which form a duplex and wherein the hybridization thermodynamics are calculated for the duplex.

13. The method as claimed in claim 1 wherein the hybridization information represents at least a section of a target and a length of at least one primer or probe complimentary to the target.

14. The method as claimed in claim 13 wherein the hybridization thermodynamics are calculated for a plurality of primers or probes complimentary to the target.

15. The method as claimed in claim 1 wherein the hybridization information represents at least a section of a target and a primer or probe.

16. The method as claimed in claim 15 wherein a length of the target is longer than a length of the primer or probe and wherein the hybridization thermodynamics are calculated for a best target/primer or target/probe complex and for competitive mismatch complexes.

17. The method as claimed in claim 14 wherein hybridization information represents at least a section of a target and a primer or probe and wherein a length of a target is longer than the length of the primer or probe and wherein the hybridization thermodynamics are calculated for a best target/primer or target/probe complex and for competitive target/primer or target/probe complexes.

18. The method as claimed in claim 2 further comprising, calculating concentration of each species in a solution at a plurality of temperatures.

19. The method as claimed in claim 18 wherein hybridization information also represents a primer or probe and wherein the length of the target is longer than a length of the primer or probe and wherein the hybridization thermodynamics are calculated for a best target/primer or target/probe complex and for competitive mismatch complexes and wherein the method further comprises calculating concentration of every species in a solution at a plurality of temperatures.

20. The method as claimed in claim 19 wherein the hybridization thermodynamics are calculated for at least two best target/primer or target/probe complexes and for their corresponding competitive mismatch complexes and wherein the method further comprises correcting for any interactions between the at least two best target/primer or target/probe complexes and their components.

21. A system for predicting nucleic acid hybridization thermodynamics, the system comprising:

a database of thermodynamics parameters;

means for receiving hybridization information which represents at least one sequence;

means for receiving correction data;

receiving a first set of data which represents hybridization conditions; and

means for calculating hybridization thermodynamics including net hybridization thermodynamics based on the hybridization information, the thermodynamic parameters, the correction data and the first set of data.

22. The system as claimed in claim 21 wherein the hybridization thermodynamics of individual single stranded, bimolecular and higher order complexes are statistically weighted in a numerical process and the equilibrium concentration of each species is output.

23. The system as claimed in claim 22 wherein the correction data includes folding correction data.

24. The system as claimed in claim 22 wherein the correction data includes linear correction data.

25. The system as claimed in claim 21 wherein the thermodynamic parameters include DNA thermodynamic parameters.

26. The system as claimed in claim 25 wherein the DNA thermodynamic parameters include dangling end parameters.

27. The system as claimed in claim 25 wherein the DNA thermodynamic parameters include coaxial stacking parameters.

28. The system as claimed in claim 25 wherein the DNA thermodynamic parameters include terminal mismatch parameters.

29. The system as claimed in claim 21 wherein the thermodynamic parameters include RNA thermodynamic parameters.

30. The system as claimed in claim 21 wherein the thermodynamic parameters include hybrid DNA/RNA thermodynamic parameters.

31. The system as claimed in claim 21 wherein the thermodynamic parameters include DNA loop thermodynamic parameters.

32. The system as claimed in claim 21 wherein the hybridization information represents top and bottom strand sequences which form a duplex and wherein the hybridization thermodynamics are calculated for the duplex.

33. The system as claimed in claim 21 wherein the hybridization information represents at least a section of a target and a length of at least one primer or probe complimentary to the target.

34. The system as claimed in claim 33 wherein the hybridization thermodynamics are calculated for a plurality of primers or probes complimentary to the target.

35. The system as claimed in claim 21 wherein the hybridization information represents at least a section of a target and a primer or probe.

36. The system as claimed in claim 35 wherein a length of the target is longer than a length of the primer or probe and wherein the hybridization thermodynamics are calculated for a best target/primer or target/probe complex and for competitive mismatch complexes.

37. The system as claimed in claim 34 wherein hybridization information represents at least a section of a target and a primer or probe and wherein a length of a target is longer than the length of the primer or probe and wherein the hybridization thermodynamics are calculated for a best target/primer or target/probe complex and for competitive target/primer or target/probe complexes.

38. The system as claimed in claim 22 further comprising means for calculating concentration of each species in a solution at a plurality of temperatures.

39. The system as claimed in claim 38 wherein hybridization information also represents a primer or probe and wherein the length of the target is longer than a length of the primer or probe and wherein the hybridization thermodynamics are calculated for a best target/primer or target/probe complex and for competitive mismatch complexes and wherein the system further comprises means for calculating concentration of every species in a solution at a plurality of temperatures.

40. The system as claimed in claim 39 wherein the hybridization thermodynamics are calculated for at least two best target/primer or target/probe complexes and for their corresponding competitive mismatch complexes and wherein the system further comprises means for correcting for any interactions between the at least two best target/primer or target/probe complexes and their components.

41. A computer-readable storage medium having stored therein a database of thermodynamics parameters and a computer program which executes the steps of:

receiving hybridization information which represents at least one sequence;

receiving correction data;

receiving a first set of data which represents hybridization conditions; and

calculating hybridization thermodynamics including net hybridization thermodynamics based on the hybridization information, the thermodynamic parameters, the correction data and the first set of data.

42. The storage medium as claimed in claim 41 wherein the hybridization thermodynamics of individual single stranded, bimolecular and higher order complexes are statistically weighted in a numerical process and the equilibrium concentration of each species is output.

43. The storage medium as claimed in claim 42 wherein the correction data includes folding correction data.

44. The storage medium as claimed in claim 42 wherein the correction data includes linear correction data.

45. The storage medium as claimed in claim 41 wherein the thermodynamic parameters include DNA thermodynamic parameters.

46. The storage medium as claimed in claim 45 wherein the DNA thermodynamic parameters include dangling end parameters.

47. The storage medium as claimed in claim 45 wherein the DNA thermodynamic parameters include coaxial stacking parameters.

48. The storage medium as claimed in claim 41 wherein the DNA thermodynamic parameters include terminal mismatch parameters.

49. The storage medium as claimed in claim 41 wherein the thermodynamic parameters include RNA thermodynamic parameters.

50. The storage medium as claimed in claim 41 wherein the thermodynamic parameters include hybrid DNA/RNA thermodynamic parameters.

51. The storage medium as claimed in claim 41 wherein the thermodynamic parameters include DNA loop thermodynamic parameters.

52. The storage medium as claimed in claim 41 wherein the hybridization information represents top and bottom strand sequences which form a duplex and wherein the hybridization thermodynamics are calculated for the duplex.

53. The storage medium as claimed in claim 41 wherein the hybridization information represents at least a section of a target and a length of at least one primer or probe complimentary to the target.

54. The storage medium as claimed in claim 53 wherein the hybridization thermodynamics are calculated for a plurality of primers or probes complimentary to the target.

55. The storage medium as claimed in claim 41 wherein the hybridization information represents at least a section of a target and a primer or probe.

56. The storage medium as claimed in claim 55 wherein a length of the target is longer than a length of the primer or probe and wherein the hybridization thermodynamics are calculated for a best target/primer or target/probe complex and for competitive mismatch complexes.

57. The storage medium as claimed in claim 54 wherein hybridization information represents at least a section of a target and a primer or probe and wherein a length of a target is longer than the length of the primer or probe and wherein the hybridization thermodynamics are calculated for a best target/primer or target/probe complex and for competitive target/primer or target/probe complexes.

58. The storage medium as claimed in claim 42 wherein the program further executes the step of calculating concentration of each species in a solution at a plurality of temperatures.

59. The storage medium as claimed in claim 58 wherein hybridization information also represents a primer or probe and wherein the length of the target is longer than a length of the primer or probe and wherein the hybridization thermodynamics are calculated for a best target/primer or target/probe complex and for competitive mismatch complexes and wherein the program

executes the step of calculating concentration of every species in a solution at a plurality of temperatures.

60. The storage medium as claimed in claim 59 wherein the hybridization thermodynamics are calculated for at least two best target/primer or target/probe complexes and for their corresponding competitive mismatch complexes and wherein the program executes the step of correcting for any interactions between the at least two best target/primer or target/probe complexes and their components.

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